

CIBT-P01-130SequenceListing  
SEQUENCE LISTING

<110> Huston, J.  
Houston, L.L.  
Ring, D.  
Oppermann, H.

<120> BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING

<130> CIBT-P01-130

<140> 09/558,741

<141> 2000-04-26

<150> 07/831,967

<151> 1992-02-06

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<223> 741F8 sFV'

<220>

<221> CDS

<222> (3)..(752)

<223>

61

<400> 1  
cc atg gcg gag atc caa ttg gtg cag tct gga cct gag ctg aag aag 47  
Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys 15  
1 5 10

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 95  
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe 20 25 30

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta 143  
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu 35 40 45

aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct 191  
Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala 50 55 60

gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc 239  
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser 65 70 75

act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca 287  
Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr 80 85 90 95

tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg 335

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Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp  
 100 105 110  
 ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct 383  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser  
 115 120 125  
 tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct 431  
 Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro  
 130 135 140  
 aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag 479  
 Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys  
 145 150 155  
 gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca 527  
 Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro  
 160 165 170 175  
 ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act 575  
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr  
 180 185 190  
 gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act 623  
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr  
 195 200 205  
 ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt 671  
 Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys  
 210 215 220  
 cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg 719  
 Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu  
 225 230 235  
 gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt 772  
 Glu Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys  
 240 245 250  
 ggggtctcgtt acgttgcgga tctcgaggct atctttacta actctttaccg taaagttctg 832  
 gctcaactgt ctgcacgcaa gcttttgcag gatattcatga gcgcttaaga tccgtcgacc 892  
 tgcaggcatg caagctt 909

<210> 2  
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<220>  
 <223> 741F8 sFv'

<400> 2

Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro  
1 5 10 15

Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr  
20 25 30

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Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys  
35 40 45

Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu  
50 55 60

Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr  
65 70 75 80

Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr  
85 90 95

Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser  
115 120 125

Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys  
130 135 140

Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala  
145 150 155 160

Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly  
165 170 175

Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly  
180 185 190

Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu  
195 200 205

Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln  
210 215 220

Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu  
225 230 235 240

Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys  
245 250

<210> 3

<211> 779

<212> DNA

<213> Artificial Sequence

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 <220>  
 <221> CDS  
 <222> (3)..(758)  
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 1 5 10 15  
 ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc 95  
 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr 20 25 30  
 gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac 143  
 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp 35 40 45  
 tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag 191  
 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln 50 55 60  
 aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act 239  
 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr 65 70 75  
 gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac 287  
 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr 80 85 90 95  
 tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt 335  
 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly 100 105 110  
 cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt 383  
 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Gly 115 120 125  
 tcc agc tgc agt gga tcc gac gtc gta atg acc cag act ccg ctg tct 431  
 Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser 130 135 140  
 ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc 479  
 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser 145 150 155  
 cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg 527  
 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu 160 165 170 175  
 caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac 575  
 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn 180 185 190  
 cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act 623  
 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Ser Gly Thr 195 200 205  
 gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc 671  
 Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile  
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210

215

220

tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc 719  
 Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly  
 225 230 235

acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc 768  
 Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys  
 240 245 250

ccgggggcatc c 779

<210> 4  
 <211> 252  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> 26-10 sFv'

<400> 4

Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly  
 1 5 10 15

Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp  
 20 25 30

Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr  
 35 40 45

Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys  
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala  
 65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
 85 90 95

Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His  
 100 105 110

Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Gly Ser  
 115 120 125

Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu  
 130 135 140

Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln  
 145 150 155 160

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Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln  
 165 170 175

Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg  
 180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr  
 210 215 220

Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr  
 225 230 235 240

Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys  
 245 250

<210> 5  
 <211> 739  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 520C9 sFv

<220>  
 <221> CDS  
 <222> (1)..(729)  
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 gag atc caa ttg gtg cag tct gga cct gag ctg aag aag cct gga gag 48  
 Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
 1 5 10 15  
 aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat 96  
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr  
 20 25 30  
 gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg 144  
 Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
 35 40 45  
 ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc 192  
 Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe  
 50 55 60  
 aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat 240  
 Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His  
 65 70 75 80  
 ttg cag atc aac aac ctc aga aat gag gac tgg gcc aca tat ttc tgt 288  
 Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys  
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85 90 95

gca aga cga ttt ggg ttt gct tac tgg ggc caa ggg act ctg gtc agt 336  
Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser  
100 105 110

gtc tct gca tcg ata tcg agc tcc tcc gga tct tca tct agc ggt tcc 384  
Val Ser Ala Ser Ile Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser  
115 120 125

agc tcg agt gga tcc gat atc cag atg acc cag tct cca tcc tcc tta 432  
Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
130 135 140

tct gcc tct ctg gga gaa aga gtc agt ctc act tgt cgg gca agt cag 480  
Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln  
145 150 155 160

gac att ggt aat agc tta acc tgg ctt cag cag gaa cca gat gga act 528  
Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr  
165 170 175

att aaa cgc ctg atc tac gcc aca tcc agt tta gat tct ggt gtc ccc 576  
Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro  
180 185 190

aaa agg ttc agt ggc agt cgg tct ggg tca gat tat tct ctc acc atc 624  
Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile  
195 200 205

agt agc ctt gag tct gaa gat ttt gta gtc tat tac tgt cta caa tat 672  
Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr  
210 215 220

gct att ttt ccg tac acg ttc gga ggg ggg acc aac ctg gaa ata aaa 720  
Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys  
225 230 235 240

cgg gct gat taatctgcag 739  
Arg Ala Asp

<210> 6  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> 520C9 sFv

<400> 6

Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr  
20 25 30

Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
35 40 45

## CIBT-P01-130SequenceListing

Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe  
50 55 60

Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His  
65 70 75 80

Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys  
85 90 95

Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser  
100 105 110

Val Ser Ala Ser Ile Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser  
115 120 125

Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
130 135 140

Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln  
145 150 155 160

Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr  
165 170 175

Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro  
180 185 190

Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile  
195 200 205

Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr  
210 215 220

Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys  
225 230 235 240

Arg Ala Asp

<210> 7  
<211> 15  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Linker 1

<400> 7



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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

<210> 8  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker 2

<400> 8

Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Ser Ser Ser Gly  
 1 5 10 15

<210> 9  
 <211> 2  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C-terminal tail

<400> 9

Ser Cys  
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<210> 10  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C-terminal tail

<400> 10

Gly Gly Gly Gly Cys  
 1 5

<210> 11  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> C-terminal tail

<400> 11

His His His His His Gly Gly Gly Gly Cys  
 1 5 10

<210> 12  
 <211> 118  
 <212> PRT  
 <213> Mus musculus

<400> 12

## CIBT-P01-130SequenceListing

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Glu Pro Gly Ala  
1 5 10 15

Ser Val Arg Ile Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30

Tyr Ile His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe  
65 70 75 80

Asn Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110

Leu Thr Val Ser Ser Lys  
115

<210> 13  
<211> 120  
<212> PRT  
<213> Mus musculus

<400> 13

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp Phe  
20 25 30

Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr Ile  
35 40 45

Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

## CIBT-P01-130SequenceListing

Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His Gly  
100 105 110

Ala Ala Ser Val Thr Val Ser Ser  
115 120

<210> 14  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Hybrid peptide

<400> 14

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30

Tyr Ile His Trp Leu Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Cys Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly His Gly Ala Ser  
100 105 110

Val Thr Val Ser Ser  
115

<210> 15  
<211> 103  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Hybrid peptide

<400> 15

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

## CIBT-P01-130SequenceListing

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Thr Asn Tyr  
20 25 30

Tyr Ile His Trp Leu Lys Gln Pro Pro Gly Arg Leu Glu Trp Ile Gly  
35 40 45

Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe Lys  
50 55 60

Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Tyr Thr His Tyr Tyr Phe  
100

<210> 16  
<211> 118  
<212> PRT  
<213> Mus musculus

<400> 16

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Ser Asn Asp  
20 25 30

Tyr Tyr Thr Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Val Phe Tyr His Gly Thr Ser Asp Asp Thr Thr Pro Leu Arg  
50 55 60

Ser Arg Val Thr Met Leu Val Asp Thr Ser Ser Lys Asn Gln Phe Ser  
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asn Leu Ile Ala Gly Cys Ile Asp Val Trp Gly Gln Gly Ser  
100 105 110

Leu Val Thr Val Ser Ser  
115

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